

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	17	(Enright Frederick).in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/08/16 11:08
L2	11310	lytic peptide	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/08/16 11:09
L3	3637	lytic peptide.clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/08/16 11:09
L4	9572	hormone.clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/08/16 11:09
L5	109	L3 and L4	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/08/16 11:10
L6	458	(gonadotropin releasing hormone). clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/08/16 11:11
L7	13	L2 and L6	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/08/16 11:11

(FILE 'HOME' ENTERED AT 11:15:25 ON 16 AUG 2006)

FILE 'MEDLINE, BIOSIS, EMBASE, CAPLUS' ENTERED AT 11:15:45 ON 16 AUG 2006

L1	1 S ENRIGHT FREDERICK/AU
L2	164 S ENRIGHT F M/AU
L3	82 DUP REM L2 (82 DUPLICATES REMOVED)
L4	4080 S LYTIC AND PEPTIDE
L5	605 S (LYTIC PEPTIDE)
L6	98825 S (CHORIONIC GONADOTROPIN)
L7	37 S L5 AND L6
L8	14 DUP REM L7 (23 DUPLICATES REMOVED)
L9	72 S L5 AND HORMONE
L10	34 DUP REM L9 (38 DUPLICATES REMOVED)

=> logoff

SCORE Search Results Details for Application 10617561 and Search Result us-10-617-561-3.p2n.rge

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This page gives you Search Results detail for the Application 10617561 and Search Result us-10-617-561-3.p2n.rge

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:33:24 ; Search time 3570.74 Seconds
(without alignments)
886.481 Million cell updates/sec

Title: US-10-617-561-3
Perfect score: 166
Sequence: 1 QHWSYGLRPGFALALKALKKKALKKKLKKALKKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102053_91/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10617561@CGN_1_1_6362@runat_11082006_102053_91 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*

6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Match	Query Length	DB	ID	Description
	1	73	44.0	379	11	AB026989	AB026989 Anguilla
c	2	73	44.0	168091	6	AC139553	AC139553 Mus muscu
	3	73	44.0	182733	6	AC123941	AC123941 Mus muscu
	4	70	42.2	1360	11	AB026991	AB026991 Anguilla
	5	67	40.4	151620	12	AC018589	AC018589 Homo sapi
c	6	67	40.4	180709	5	AC018557	AC018557 Homo sapi
c	7	67	40.4	188460	5	AC010542	AC010542 Homo sapi
	8	67	40.4	244067	12	AC094761	AC094761 Rattus no
	9	67	40.4	253041	12	AC124839	AC124839 Rattus no
	10	66.5	40.1	110000	15	AE016877_47	Continuation (48 o
	11	66	39.8	227	6	AJ966357	AJ966357 Cryptomys
	12	66	39.8	551	11	AF046801	AF046801 Sparus au
	13	66	39.8	652	11	AF188754	AF188754 Rana cate
c	14	65.5	39.5	110000	15	AP006716_19	Continuation (20 o
	15	65	39.2	54	2	A21730	A21730 TraTp LHRH
	16	65	39.2	728	4	DQ180313	DQ180313 Fragaria
	17	64.5	38.9	408	14	TGU63326	U63326 Tupaia glis
c	18	64	38.6	66	2	DD179332	DD179332 Albumin F
	19	64	38.6	68	2	DD179331	DD179331 Albumin F
	20	64	38.6	191	2	CS211821	CS211821 Sequence
	21	64	38.6	191	2	CS215463	CS215463 Sequence
	22	64	38.6	191	6	MAU91938	U91938 Mesocricetu
	23	64	38.6	395	11	DQ074693	DQ074693 Paralicht
	24	64	38.6	2468	5	BC053878	BC053878 Homo sapi
	25	64	38.6	132701	5	AC078867	AC078867 Homo sapi
	26	64	38.6	160302	12	AC068818	AC068818 Homo sapi
	27	64	38.6	274710	12	AC131884	AC131884 Rattus no
c	28	63.5	38.3	110000	4	AE017346_11	Continuation (12 o
c	29	63.5	38.3	110000	4	AE017346_12	Continuation (13 o
	30	63	38.0	30	2	AR054437	AR054437 Sequence
	31	63	38.0	30	2	AR081027	AR081027 Sequence
	32	63	38.0	30	2	BD009868	BD009868 GnRH-leuk
	33	63	38.0	30	2	BD205494	BD205494 Method of
	34	63	38.0	30	2	BD268058	BD268058 Methods f
	35	63	38.0	30	2	I08473	I08473 Sequence 10
	36	63	38.0	30	2	AR282597	AR282597 Sequence
	37	63	38.0	30	2	I89772	I89772 Sequence 1
	38	63	38.0	31	2	A78525	A78525 Sequence 3
	39	63	38.0	31	2	I72588	I72588 Sequence 3
	40	63	38.0	32	2	I06760	I06760 Sequence 2
	41	63	38.0	36	2	A78523	A78523 Sequence 1

SCORE Search Results Details for Application 10617561 and Search Result us-10-617-561-3.p2n.rng.

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This page gives you Search Results detail for the Application 10617561 and Search Result us-10-617-561-3.p2n.rnq.

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OM protein - nucleic search, using frame plus p2n model

```
Run on:      August 12, 2006, 09:32:04 ; Search time 332.409 Seconds
              (without alignments)
              1038.259 Million cell updates/sec
```

```
Title:          US-10-617-561-3
Perfect score:  166
Sequence:       1 QHWSYGLRPGFALALKALKKALKKKLKKALKKKAL 33
```

```

Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext  7.0

```

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102051_79/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561_@CGN_1_1_1975_@runat_11082006_102051_79 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

```
Database :      N_Geneseq_8:*
           1:    geneseqn1980s:*
```

2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query						Description
	No.	Score	Match	Length	DB	ID	
	1	67.5	40.7	420	14	ADV60377	Adv60377 DNA seque
	2	65.5	39.5	462	14	ADV60378	Adv60378 DNA seque
	3	65	39.2	774	2	AAQ11000	Aaq11000 Plasmid p
c	4	64	38.6	66	10	ADF15466	Adf15466 Human alb
	5	64	38.6	68	10	ADF15465	Adf15465 Human alb
	6	64	38.6	191	14	AEE11629	Aee11629 Hamster c
	7	64	38.6	191	14	AEE15271	Aee15271 Hamster S
	8	63	38.0	30	2	AAV61528	Aav61528 Nucleic a
	9	63	38.0	30	2	AAV45189	Aav45189 Peptide h
	10	63	38.0	30	3	AAZ55701	Aaz55701 DNA encod
	11	63	38.0	30	3	AAZ46401	Aaz46401 DNA encod
	12	63	38.0	30	10	ADK82638	Adk82638 LHRH(M) v
	13	63	38.0	30	15	AEF02851	Aef02851 DNA encod
	14	63	38.0	30	15	AEF52728	Aef52728 Gonadotro
	15	63	38.0	30	15	AEF73587	Aef73587 Human GnR
	16	63	38.0	32	2	AAQ03656	Aaq03656 Luteinisi
	17	63	38.0	34	3	AAZ90140	Aaz90140 Luteinisi
	18	63	38.0	36	2	AAQ54393	Aaq54393 E. coli f
	19	63	38.0	39	2	AAQ41319	Aaq41319 GnRH DNA
	20	63	38.0	42	2	AAQ54392	Aaq54392 E. coli f
	21	63	38.0	44	8	ABZ80017	Abz80017 Gonadotro
	22	63	38.0	44	10	ADF15463	Adf15463 Human alb
	23	63	38.0	45	2	AAQ54394	Aaq54394 E. coli f
c	24	63	38.0	45	10	ADF15464	Adf15464 Human alb
	25	63	38.0	46	13	ADW64314	Adw64314 (GnRH) 1-h
c	26	63	38.0	52	10	ADK82631	Adk82631 LHRH(M) g
	27	63	38.0	53	10	ADK82630	Adk82630 LHRH(M) g
	28	63	38.0	54	14	AEG01877	Aeg01877 Region of
	29	63	38.0	54	15	AEF52724	Aef52724 GnRH-TNFa
	30	63	38.0	122	13	ADS91431	Ads91431 Nucleotid
	31	63	38.0	122	13	ADT62560	Adt62560 Polynucle
	32	63	38.0	122	13	ADU66752	Adu66752 Signal pe
	33	63	38.0	147	2	AAT37178	Aat37178 GnRH 4 mu
	34	63	38.0	147	2	AAV61529	Aav61529 Nucleic a
	35	63	38.0	147	2	AAV45190	Aav45190 Peptide h
	36	63	38.0	147	3	AAZ55702	Aaz55702 DNA encod
	37	63	38.0	147	3	AAZ46402	Aaz46402 DNA encod

SCORE Search Results Details for Application 10617561 and Search Result us-10-617-561-3.p2n.rni.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:51:34 ; Search time 104.299 Seconds
(without alignments)
888.020 Million cell updates/sec

Title: US-10-617-561-3
Perfect score: 166
Sequence: 1 QHWSYGLRPGFALALKALKKALKKALKKALKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102057_179/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss06p -USER=US10617561@CGN_1_1_529@runat_11082006_102057_179 -NCPU=6
-ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
c	1	69	41.6	60	3	US-08-897-527-3	Sequence 3, Appli
c	2	69	41.6	60	3	US-09-072-508-3	Sequence 3, Appli
c	3	66.5	40.1	75	3	US-08-897-527-2	Sequence 2, Appli
c	4	66.5	40.1	75	3	US-09-072-508-2	Sequence 2, Appli
	5	65	39.2	54	2	US-07-690-983D-19	Sequence 19, Appl
c	6	63.5	38.3	60	3	US-08-897-527-4	Sequence 4, Appli
c	7	63.5	38.3	60	3	US-09-072-508-4	Sequence 4, Appli
c	8	63	38.0	30	2	US-07-690-983D-33	Sequence 33, Appl
	9	63	38.0	30	2	US-08-387-156-1	Sequence 1, Appli
	10	63	38.0	30	2	US-08-694-865-1	Sequence 1, Appli
	11	63	38.0	30	2	US-08-878-748-1	Sequence 1, Appli
	12	63	38.0	30	3	US-09-124-491-1	Sequence 1, Appli
	13	63	38.0	30	3	US-09-383-912-1	Sequence 1, Appli
	14	63	38.0	31	2	US-08-453-588-3	Sequence 3, Appli
	15	63	38.0	31	3	US-08-521-079-3	Sequence 3, Appli
	16	63	38.0	36	2	US-08-453-588-1	Sequence 1, Appli
	17	63	38.0	36	2	US-08-453-588-28	Sequence 28, Appl
	18	63	38.0	36	3	US-08-521-079-1	Sequence 1, Appli
	19	63	38.0	36	3	US-08-521-079-28	Sequence 28, Appl
	20	63	38.0	39	2	US-07-960-932-4	Sequence 4, Appli
c	21	63	38.0	39	2	US-07-960-932-5	Sequence 5, Appli
	22	63	38.0	39	2	US-08-453-588-5	Sequence 5, Appli
	23	63	38.0	39	2	US-08-455-970A-5	Sequence 5, Appli
c	24	63	38.0	39	2	US-08-455-970A-6	Sequence 6, Appli
	25	63	38.0	39	3	US-08-521-079-5	Sequence 5, Appli
	26	63	38.0	39	3	US-08-976-566-5	Sequence 5, Appli
c	27	63	38.0	39	3	US-08-976-566-6	Sequence 6, Appli
	28	63	38.0	42	2	US-08-453-588-7	Sequence 7, Appli
	29	63	38.0	42	2	US-08-453-588-11	Sequence 11, Appl
	30	63	38.0	42	2	US-08-453-588-27	Sequence 27, Appl
	31	63	38.0	42	3	US-08-521-079-7	Sequence 7, Appli
	32	63	38.0	42	3	US-08-521-079-11	Sequence 11, Appl
	33	63	38.0	42	3	US-08-521-079-27	Sequence 27, Appl
	34	63	38.0	45	2	US-08-453-588-29	Sequence 29, Appl
	35	63	38.0	45	3	US-08-521-079-29	Sequence 29, Appl
	36	63	38.0	48	2	US-08-453-588-9	Sequence 9, Appli
	37	63	38.0	48	2	US-08-453-588-30	Sequence 30, Appl
	38	63	38.0	48	3	US-08-521-079-9	Sequence 9, Appli
	39	63	38.0	48	3	US-08-521-079-30	Sequence 30, Appl
	40	63	38.0	51	2	US-08-453-588-13	Sequence 13, Appl
	41	63	38.0	51	3	US-08-521-079-13	Sequence 13, Appl
	42	63	38.0	54	2	US-08-453-588-15	Sequence 15, Appl

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:58:24 ; Search time 1105.86 Seconds
(without alignments)
550.013 Million cell updates/sec

Title: US-10-617-561-3
Perfect score: 166
Sequence: 1 QHWSYGLRPGFALALKALKKKLKKALKKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102100_235/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10617561_CGN_1_1_5513_runat_11082006_102100_235 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*

```

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID		Description
	1	70	42.2	4009	8	US-10-424-599-80837	Sequence 80837, A
c	2	69	41.6	60	3	US-09-524-974-3	Sequence 3, Appli
c	3	66.5	40.1	75	3	US-09-524-974-2	Sequence 2, Appli
c	4	64	38.6	66	10	US-10-775-204-750	Sequence 750, App
	5	64	38.6	68	10	US-10-775-204-749	Sequence 749, App
	6	64	38.6	191	16	US-11-128-061-1140	Sequence 1140, Ap
	7	64	38.6	191	16	US-11-128-061-4782	Sequence 4782, Ap
	8	64	38.6	191	16	US-11-128-049-1140	Sequence 1140, Ap
	9	64	38.6	191	16	US-11-128-049-4782	Sequence 4782, Ap
c	10	63.5	38.3	60	3	US-09-524-974-4	Sequence 4, Appli
	11	63	38.0	30	3	US-09-019-010-1	Sequence 1, Appli
	12	63	38.0	30	3	US-09-305-924-8	Sequence 8, Appli
	13	63	38.0	34	3	US-09-746-945-9	Sequence 9, Appli
	14	63	38.0	44	10	US-10-775-204-747	Sequence 747, App
c	15	63	38.0	45	10	US-10-775-204-748	Sequence 748, App
	16	63	38.0	65	3	US-09-524-974-7	Sequence 7, Appli
c	17	63	38.0	66	3	US-09-524-974-8	Sequence 8, Appli
	18	63	38.0	67	3	US-09-524-974-5	Sequence 5, Appli
c	19	63	38.0	69	3	US-09-524-974-6	Sequence 6, Appli
	20	63	38.0	122	9	US-10-746-943-45	Sequence 45, Appl
	21	63	38.0	147	3	US-09-019-010-3	Sequence 3, Appli
	22	63	38.0	147	3	US-09-305-924-10	Sequence 10, Appl
	23	63	38.0	249	10	US-10-498-346-2	Sequence 2, Appli
	24	63	38.0	279	10	US-10-775-204-53	Sequence 53, Appl
	25	63	38.0	279	10	US-10-775-204-54	Sequence 54, Appl
	26	63	38.0	470	7	US-10-007-926A-278	Sequence 278, App
	27	63	38.0	470	10	US-10-498-346-35	Sequence 35, Appl
	28	63	38.0	2088	3	US-09-305-924-12	Sequence 12, Appl
c	29	63	38.0	2480	6	US-10-027-632-111864	Sequence 111864,
c	30	63	38.0	2480	6	US-10-027-632-111865	Sequence 111865,
c	31	63	38.0	2480	7	US-10-027-632-111864	Sequence 111864,
c	32	63	38.0	2480	7	US-10-027-632-111865	Sequence 111865,
	33	63	38.0	2481	6	US-10-027-632-103403	Sequence 103403,
	34	63	38.0	2481	6	US-10-027-632-103404	Sequence 103404,
	35	63	38.0	2481	7	US-10-027-632-103403	Sequence 103403,

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:59:05 ; Search time 134.891 Seconds
(without alignments)
582.767 Million cell updates/sec

Title: US-10-617-561-3
Perfect score: 166
Sequence: 1 QHWSYGLRPGFALALKALKKKLKKALKKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 4400442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102102_304/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561_CGN_1_1_661_runat_11082006_102102_304 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*

```

1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	64	38.6	2468	8	US-11-266-748A-27808	Sequence 27808, A
	2	63	38.0	716	8	US-11-266-748A-80207	Sequence 80207, A
c	3	63	38.0	716	8	US-11-266-748A-133018	Sequence 133018,
	4	63	38.0	1000	8	US-11-266-748A-393754	Sequence 393754,
c	5	63	38.0	1000	8	US-11-266-748A-464800	Sequence 464800,
	6	61.5	37.0	1901	9	US-11-218-305-20231	Sequence 20231, A
	7	60	36.1	3602	6	US-10-449-902-12825	Sequence 12825, A
c	8	59	35.5	301692	8	US-11-266-748A-28776	Sequence 28776, A
	9	58.5	35.2	1000	8	US-11-266-748A-119142	Sequence 119142,
c	10	58.5	35.2	1000	8	US-11-266-748A-161306	Sequence 161306,
	11	58.5	35.2	1000	8	US-11-266-748A-294459	Sequence 294459,
c	12	58.5	35.2	1000	8	US-11-266-748A-345888	Sequence 345888,
	13	58.5	35.2	1000	8	US-11-266-748A-401662	Sequence 401662,
	14	58.5	35.2	1000	8	US-11-266-748A-401663	Sequence 401663,
	15	58.5	35.2	1000	8	US-11-266-748A-406743	Sequence 406743,
c	16	58.5	35.2	1000	8	US-11-266-748A-472708	Sequence 472708,
c	17	58.5	35.2	1000	8	US-11-266-748A-472709	Sequence 472709,
c	18	58.5	35.2	1000	8	US-11-266-748A-477789	Sequence 477789,
	19	58	34.9	442	9	US-11-348-413-2009	Sequence 2009, Ap
c	20	57.5	34.6	415	8	US-11-266-748A-61593	Sequence 61593, A
	21	57.5	34.6	700	8	US-11-266-748A-480122	Sequence 480122,
	22	57.5	34.6	2218	8	US-11-293-697-2174	Sequence 2174, Ap
	23	57	34.3	816	8	US-11-266-748A-354233	Sequence 354233,
	24	57	34.3	816	8	US-11-266-748A-384829	Sequence 384829,
c	25	57	34.3	816	8	US-11-266-748A-437612	Sequence 437612,
	26	57	34.3	942	8	US-11-266-748A-354234	Sequence 354234,
	27	57	34.3	942	8	US-11-266-748A-384830	Sequence 384830,
c	28	57	34.3	942	8	US-11-266-748A-437613	Sequence 437613,
	29	57	34.3	1007	8	US-11-266-748A-189883	Sequence 189883,
	30	57	34.3	1114	8	US-11-266-748A-82712	Sequence 82712, A
c	31	57	34.3	1114	8	US-11-266-748A-135523	Sequence 135523,
	32	57	34.3	1318	6	US-10-374-780A-733	Sequence 733, App
	33	57	34.3	1852	8	US-11-293-697-147	Sequence 147, App
	34	57	34.3	2029	8	US-11-266-748A-31531	Sequence 31531, A
	35	57	34.3	3740	9	US-11-226-554-18	Sequence 18, Appl
	36	57	34.3	3740	9	US-11-248-718-18	Sequence 18, Appl
	37	56.5	34.0	95662	8	US-11-266-748A-60952	Sequence 60952, A
	38	55	33.1	1000	8	US-11-266-748A-202377	Sequence 202377,
	39	55	33.1	1000	8	US-11-266-748A-223820	Sequence 223820,
	40	55	33.1	1566	9	US-11-348-413-7624	Sequence 7624, Ap
	41	55	33.1	1586	9	US-11-218-305-14783	Sequence 14783, A

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:35:25 ; Search time 3516.55 Seconds
(without alignments)
787.138 Million cell updates/sec

Title: US-10-617-561-3
Perfect score: 166
Sequence: 1 QHWSYGLRPGFALALKALKKALKKKLKKALKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102055_128/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561@CGN_1_1_17145@runat_11082006_102055_128 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*

2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_hlc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	No.	Score	Query Match	Length	DB	ID	
c	1	74	44.6	343	8	CX142641	CX142641 1282240 N
	2	74	44.6	597	8	CX150503	CX150503 1290824 N
c	3	74	44.6	597	8	CX150504	CX150504 1290825 N
c	4	74	44.6	627	8	CX145419	CX145419 1285211 N
c	5	74	44.6	760	8	CX136492	CX136492 1275495 N
c	6	70	42.2	549	9	CX717617	CX717617 1334124 N
c	7	69.5	41.9	328	7	BE904288	BE904288 601494556
	8	69	41.6	626	8	CX145418	CX145418 1285210 N
c	9	69	41.6	723	8	CX150645	CX150645 1290991 N
c	10	67	40.4	727	8	CX152130	CX152130 1292617 N
	11	65	39.2	297	8	CV507819	CV507819 kc06f10.y
c	12	65	39.2	635	8	CX151883	CX151883 1292349 N
c	13	65	39.2	656	5	CK013788	CK013788 30991sice
c	14	65	39.2	899	10	DT784124	DT784124 127466847
	15	64	38.6	227	4	CB530101	CB530101 690870 MA
c	16	64	38.6	327	5	CF331667	CF331667 NACL--07-
	17	64	38.6	402	5	CJ201010	CJ201010 CJ201010
	18	64	38.6	403	5	CJ202177	CJ202177 CJ202177
	19	64	38.6	451	5	CI070753	CI070753 CI070753
	20	64	38.6	483	6	AK139480	AK139480 Mus muscu
	21	64	38.6	494	5	CJ059442	CJ059442 CJ059442
	22	64	38.6	556	9	CX763652	CX763652 AGENCOURT
c	23	64	38.6	732	13	CZ895839	CZ895839 226_1_123
c	24	64	38.6	761	1	AI667294	AI667294 fc38h01.x
	25	63.5	38.3	487	5	CJ253444	CJ253444 CJ253444
	26	63	38.0	153	14	AY399439	AY399439 Pan trogl
	27	63	38.0	291	14	AY399438	AY399438 Homo sapi
	28	63	38.0	291	14	AY399440	AY399440 Mus muscu
	29	63	38.0	319	7	BE663128	BE663128 116717 MA
c	30	63	38.0	344	2	BG943943	BG943943 ax44a10.x
c	31	63	38.0	395	7	BF511931	BF511931 UI-H-BI4-
c	32	63	38.0	404	1	AI341355	AI341355 qx85f08.x
c	33	63	38.0	421	1	AA043996	AA043996 zk58h08.s
	34	63	38.0	428	12	CG607997	CG607997 OST287671
c	35	63	38.0	440	1	AI014477	AI014477 os34e10.s
c	36	63	38.0	526	7	BF511936	BF511936 UI-H-BI4-
c	37	63	38.0	611	9	DN051020	DN051020 JGI_CABA6
	38	63	38.0	612	9	DN051021	DN051021 JGI_CABA6

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:33:24 ; Search time 3570.74 Seconds
(without alignments)
886.481 Million cell updates/sec

Title: US-10-617-561-4
Perfect score: 166
Sequence: 1 FALALKALKKALKKLKKALKKALQHWSYGLRPG 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102053_91/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10617561@CGN_1_1_6362@runat_11082006_102053_91 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*

6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
c	1	69.5	41.9	209085	12	AC121211	AC121211 Rattus no
c	2	69.5	41.9	222057	12	AC136191	AC136191 Rattus no
	3	69.5	41.9	235305	12	AC095540	AC095540 Rattus no
	4	67.5	40.7	110000	15	AE016877_47	Continuation (48 o
	5	67	40.4	36	2	I72599	I72599 Sequence 28
	6	67	40.4	42	2	A78533	A78533 Sequence 11
	7	67	40.4	42	2	I72592	I72592 Sequence 11
	8	67	40.4	42	2	I72598	I72598 Sequence 27
	9	67	40.4	44	2	DD179329	DD179329 Albumin F
c	10	67	40.4	45	2	DD179330	DD179330 Albumin F
	11	67	40.4	48	2	A78531	A78531 Sequence 9
	12	67	40.4	48	2	I72591	I72591 Sequence 9
	13	67	40.4	1635	2	AR054441	AR054441 Sequence
	14	67	40.4	1635	2	AR081031	AR081031 Sequence
	15	67	40.4	1635	2	BD009872	BD009872 GnRH-leuk
	16	67	40.4	1635	2	AR282601	AR282601 Sequence
	17	67	40.4	1635	2	I89776	I89776 Sequence 9
	18	67	40.4	2088	2	BD205496	BD205496 Method of
	19	67	40.4	2088	2	BD268060	BD268060 Methods f
	20	67	40.4	2102	2	AR054444	AR054444 Sequence
	21	67	40.4	2102	2	BD009875	BD009875 GnRH-leuk
	22	67	40.4	2102	2	AR282604	AR282604 Sequence
	23	67	40.4	2817	2	I12265	I12265 Sequence 9
	24	67	40.4	2817	2	I80037	I80037 Sequence 11
	25	67	40.4	2817	2	AR584229	AR584229 Sequence
	26	67	40.4	2934	2	AR054440	AR054440 Sequence
	27	67	40.4	2934	2	AR081030	AR081030 Sequence
	28	67	40.4	2934	2	BD009871	BD009871 GnRH-leuk
	29	67	40.4	2934	2	AR282600	AR282600 Sequence
	30	67	40.4	2934	2	I89775	I89775 Sequence 7
	31	66	39.8	51	2	A21728	A21728 TraTp LHRH
	32	65	39.2	122034	12	CR382371	CR382371 Danio rer
	33	65	39.2	154608	12	AC073620	AC073620 Homo sapi
	34	65	39.2	178473	5	AL449344	AL449344 Human DNA
c	35	64.5	38.9	152135	5	AC148057	AC148057 Callicebu
	36	64	38.6	36	2	E63231	E63231 Fused prote
	37	64	38.6	36	2	AR691430	AR691430 Sequence
c	38	64	38.6	68040	12	AP002082	AP002082 Homo sapi
c	39	64	38.6	118645	12	AP001940	AP001940 Homo sapi
	40	64	38.6	140289	11	BX005458	BX005458 Zebrafish
	41	64	38.6	207077	12	AC097903	AC097903 Rattus no

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:32:04 ; Search time 332.409 Seconds
(without alignments)
1038.259 Million cell updates/sec

Title: US-10-617-561-4
Perfect score: 166
Sequence: 1 FALALKALKKKALKKKALKKKALQHWSYGLRPG 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102051_79/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561@CGN_1_1_1975@runat_11082006_102051_79 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
1: geneseqn1980s:*

2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	
1	69	41.6	420	14	ADV60377	Adv60377 DNA seque	
2	69	41.6	462	14	ADV60378	Adv60378 DNA seque	
3	69	41.6	774	2	AAQ10999	Aaq10999 Plasmid p	
4	68	41.0	54	15	AEF52724	Aef52724 GnRH-TNFa	
5	67	40.4	36	2	AAQ54393	Aaq54393 E. coli f	
6	67	40.4	42	2	AAQ54392	Aaq54392 E. coli f	
7	67	40.4	44	10	ADF15463	Adf15463 Human alb	
c 8	67	40.4	45	10	ADF15464	Adf15464 Human alb	
9	67	40.4	213	12	ADH74978	Adh74978 Gonadotro	
10	67	40.4	1635	2	AAT37177	Aat37177 LKT-GnRH	
11	67	40.4	1635	2	AAV61532	Aav61532 Nucleic a	
12	67	40.4	2088	2	AAV61535	Aav61535 Nucleic a	
13	67	40.4	2088	3	AAZ55700	Aaz55700 DNA encod	
14	67	40.4	2088	3	AAZ46400	Aaz46400 Gonadotro	
15	67	40.4	2102	15	AEF02855	Aef02855 DNA encod	
16	67	40.4	2817	2	AAQ41322	Aaq41322 GnRH-leuk	
17	67	40.4	2934	2	AAT37176	Aat37176 LKT-GnRH	
18	67	40.4	2934	2	AAV61531	Aav61531 Nucleic a	
19	65.5	39.5	762	2	AAQ10997	Aaq10997 Plasmid p	
20	65	39.2	34	3	AAZ90140	Aaz90140 Luteinisi	
21	65	39.2	528	15	AEF73594	Aef73594 Human GnR	
22	65	39.2	531	15	AEF52720	Aef52720 GnRH-TNFa	
23	65	39.2	660	15	AEF73592	Aef73592 Human GnR	
24	64	38.6	36	3	AAA50543	Aaa50543 Gonadotro	
25	64	38.6	762	2	AAQ11018	Aaq11018 Plasmid p	
26	63.5	38.3	265	3	AAC71581	Aac71581 Single nu	
27	63.5	38.3	265	3	AAC71572	Aac71572 Single nu	
28	63.5	38.3	265	3	AAC71584	Aac71584 Single nu	
29	63.5	38.3	301	13	ACN37112	Acn37112 Human per	
30	63.5	38.3	301	13	ACN37111	Acn37111 Human per	
31	63.5	38.3	679	4	AAS15364	Aas15364 cDNA enco	
32	63.5	38.3	1512	1	AAN60962	Aan60962 Sequence	
33	63.5	38.3	7224	9	AAL62562	Aal62562 Human gon	
34	63	38.0	30	2	AAV61528	Aav61528 Nucleic a	
35	63	38.0	30	2	AAV45189	Aav45189 Peptide h	
36	63	38.0	30	3	AAZ55701	Aaz55701 DNA encod	
37	63	38.0	30	3	AAZ46401	Aaz46401 DNA encod	

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:51:34 ; Search time 104.299 Seconds
(without alignments)
888.020 Million cell updates/sec

Title: US-10-617-561-4
Perfect score: 166
Sequence: 1 FALALKALKKALKKKLKKALKKKALQHWSYGLRPG 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102057_179/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss06p -USER=US10617561_CGN_1_1_529@runat_11082006_102057_179 -NCPU=6
-ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	67	40.4	36	2	US-08-453-588-28	Sequence 28, Appl
2	67	40.4	36	3	US-08-521-079-28	Sequence 28, Appl
3	67	40.4	42	2	US-08-453-588-11	Sequence 11, Appl
4	67	40.4	42	2	US-08-453-588-27	Sequence 27, Appl
5	67	40.4	42	3	US-08-521-079-11	Sequence 11, Appl
6	67	40.4	42	3	US-08-521-079-27	Sequence 27, Appl
7	67	40.4	48	2	US-08-453-588-9	Sequence 9, Appli
8	67	40.4	48	3	US-08-521-079-9	Sequence 9, Appli
9	67	40.4	1635	2	US-08-387-156-9	Sequence 9, Appli
10	67	40.4	1635	2	US-08-694-865-9	Sequence 9, Appli
11	67	40.4	1635	2	US-08-878-748-9	Sequence 9, Appli
12	67	40.4	1635	3	US-09-124-491-9	Sequence 9, Appli
13	67	40.4	1635	3	US-09-383-912-9	Sequence 9, Appli
14	67	40.4	2102	2	US-08-694-865-15	Sequence 15, Appl
15	67	40.4	2102	3	US-09-124-491-15	Sequence 15, Appl
16	67	40.4	2102	3	US-09-383-912-15	Sequence 15, Appl
17	67	40.4	2817	2	US-07-960-932-9	Sequence 9, Appli
18	67	40.4	2817	2	US-08-455-970A-11	Sequence 11, Appl
19	67	40.4	2817	3	US-08-976-566-11	Sequence 11, Appl
20	67	40.4	2934	2	US-08-387-156-7	Sequence 7, Appli
21	67	40.4	2934	2	US-08-694-865-7	Sequence 7, Appli
22	67	40.4	2934	2	US-08-878-748-7	Sequence 7, Appli
23	67	40.4	2934	3	US-09-124-491-7	Sequence 7, Appli
24	67	40.4	2934	3	US-09-383-912-7	Sequence 7, Appli
25	66	39.8	51	2	US-07-690-983D-17	Sequence 17, Appl
26	65	39.2	67	3	US-08-897-527-5	Sequence 5, Appli
27	65	39.2	67	3	US-09-072-508-5	Sequence 5, Appli
28	64	38.6	36	3	US-09-506-078-3	Sequence 3, Appli
29	64	38.6	65	3	US-08-897-527-7	Sequence 7, Appli
30	64	38.6	65	3	US-09-072-508-7	Sequence 7, Appli
c 31	63	38.0	30	2	US-07-690-983D-33	Sequence 33, Appl
32	63	38.0	30	2	US-08-387-156-1	Sequence 1, Appli
33	63	38.0	30	2	US-08-694-865-1	Sequence 1, Appli
34	63	38.0	30	2	US-08-878-748-1	Sequence 1, Appli
35	63	38.0	30	3	US-09-124-491-1	Sequence 1, Appli
36	63	38.0	30	3	US-09-383-912-1	Sequence 1, Appli
37	63	38.0	31	2	US-08-453-588-3	Sequence 3, Appli
38	63	38.0	31	3	US-08-521-079-3	Sequence 3, Appli
39	63	38.0	36	2	US-08-453-588-1	Sequence 1, Appli
40	63	38.0	36	3	US-08-521-079-1	Sequence 1, Appli
41	63	38.0	39	2	US-07-960-932-4	Sequence 4, Appli
c 42	63	38.0	39	2	US-07-960-932-5	Sequence 5, Appli

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:58:24 ; Search time 1105.86 Seconds
(without alignments)
550.013 Million cell updates/sec

Title: US-10-617-561-4
Perfect score: 166
Sequence: 1 FALALKALKKALKKLKKALKKALQHWSYGLRPG 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102100_235/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10617561_CGN_1_1_5513_runat_11082006_102100_235 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*


```

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
c	1	67	40.4	44	10	US-10-775-204-747	Sequence 747, App
	2	67	40.4	45	10	US-10-775-204-748	Sequence 748, App
	3	67	40.4	2088	3	US-09-305-924-12	Sequence 12, Appl
	4	66	39.8	700	8	US-10-424-599-98645	Sequence 98645, A
	5	65	39.2	34	3	US-09-746-945-9	Sequence 9, Appli
	6	65	39.2	67	3	US-09-524-974-5	Sequence 5, Appli
	7	65	39.2	2436	9	US-10-425-115-87003	Sequence 87003, A
	8	64	38.6	36	10	US-10-999-363-3	Sequence 3, Appli
	9	64	38.6	65	3	US-09-524-974-7	Sequence 7, Appli
c	10	63.5	38.3	2480	6	US-10-027-632-111864	Sequence 111864,
c	11	63.5	38.3	2480	6	US-10-027-632-111865	Sequence 111865,
c	12	63.5	38.3	2480	7	US-10-027-632-111864	Sequence 111864,
c	13	63.5	38.3	2480	7	US-10-027-632-111865	Sequence 111865,
	14	63.5	38.3	2481	6	US-10-027-632-103403	Sequence 103403,
	15	63.5	38.3	2481	6	US-10-027-632-103404	Sequence 103404,
	16	63.5	38.3	2481	7	US-10-027-632-103403	Sequence 103403,
	17	63.5	38.3	2481	7	US-10-027-632-103404	Sequence 103404,
	18	63.5	38.3	7224	10	US-10-498-346-33	Sequence 33, Appl
	19	63	38.0	30	3	US-09-019-010-1	Sequence 1, Appli
	20	63	38.0	30	3	US-09-305-924-8	Sequence 8, Appli
c	21	63	38.0	60	3	US-09-524-974-3	Sequence 3, Appli
c	22	63	38.0	60	3	US-09-524-974-4	Sequence 4, Appli
c	23	63	38.0	66	3	US-09-524-974-8	Sequence 8, Appli
c	24	63	38.0	66	10	US-10-775-204-750	Sequence 750, App
	25	63	38.0	68	10	US-10-775-204-749	Sequence 749, App
c	26	63	38.0	69	3	US-09-524-974-6	Sequence 6, Appli
c	27	63	38.0	75	3	US-09-524-974-2	Sequence 2, Appli
	28	63	38.0	76	10	US-10-999-363-5	Sequence 5, Appli
	29	63	38.0	122	9	US-10-746-943-45	Sequence 45, Appl
	30	63	38.0	147	3	US-09-019-010-3	Sequence 3, Appli
	31	63	38.0	147	3	US-09-305-924-10	Sequence 10, Appl
	32	63	38.0	191	16	US-11-128-061-1140	Sequence 1140, Ap
	33	63	38.0	191	16	US-11-128-061-4782	Sequence 4782, Ap
	34	63	38.0	191	16	US-11-128-049-1140	Sequence 1140, Ap
	35	63	38.0	191	16	US-11-128-049-4782	Sequence 4782, Ap

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:59:05 ; Search time 134.891 Seconds
(without alignments)
582.767 Million cell updates/sec

Title: US-10-617-561-4
Perfect score: 166
Sequence: 1 FALALKALKKALKKLKKALKKALQHWSYGLRPG 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 4400442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102102_304/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561_@CGN_1_1_661_@runat_11082006_102102_304 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	64	38.6	1286	6	US-10-953-349-24990	Sequence 24990, A
	2	64	38.6	1286	9	US-11-056-355B-58475	Sequence 58475, A
	3	63.5	38.3	716	8	US-11-266-748A-80207	Sequence 80207, A
c	4	63.5	38.3	716	8	US-11-266-748A-133018	Sequence 133018,
	5	63.5	38.3	1000	8	US-11-266-748A-393754	Sequence 393754,
c	6	63.5	38.3	1000	8	US-11-266-748A-464800	Sequence 464800,
	7	62.5	37.7	1830	8	US-11-266-748A-61336	Sequence 61336, A
	8	61.5	37.0	1000	8	US-11-266-748A-203292	Sequence 203292,
	9	59	35.5	442	9	US-11-348-413-2009	Sequence 2009, Ap
c	10	59	35.5	185035	8	US-11-266-748A-59932	Sequence 59932, A
	11	58	34.9	887	9	US-11-218-305-14334	Sequence 14334, A
c	12	58	34.9	1000	8	US-11-266-748A-208784	Sequence 208784,
	13	58	34.9	1000	8	US-11-266-748A-390286	Sequence 390286,
c	14	58	34.9	1000	8	US-11-266-748A-481004	Sequence 481004,
	15	58	34.9	2525	6	US-10-449-902-16046	Sequence 16046, A
	16	58	34.9	2951	9	US-11-218-305-14934	Sequence 14934, A
c	17	57.5	34.6	1000	8	US-11-266-748A-394044	Sequence 394044,
c	18	57.5	34.6	1000	8	US-11-266-748A-397039	Sequence 397039,
	19	57.5	34.6	1000	8	US-11-266-748A-465090	Sequence 465090,
	20	57.5	34.6	1000	8	US-11-266-748A-468085	Sequence 468085,
	21	57	34.3	2166	6	US-10-449-902-22182	Sequence 22182, A
	22	57	34.3	2167	6	US-10-449-902-24472	Sequence 24472, A
	23	57	34.3	2531	6	US-10-449-902-22386	Sequence 22386, A
	24	57	34.3	2563	6	US-10-449-902-2818	Sequence 2818, Ap
	25	55	33.1	1000	8	US-11-266-748A-406296	Sequence 406296,
c	26	55	33.1	1000	8	US-11-266-748A-477342	Sequence 477342,
	27	55	33.1	1452	6	US-10-449-902-9932	Sequence 9932, Ap
	28	54.5	32.8	402	8	US-11-266-748A-50389	Sequence 50389, A
	29	54.5	32.8	602	9	US-11-056-355B-95847	Sequence 95847, A
	30	54.5	32.8	667	9	US-11-218-305-7617	Sequence 7617, Ap
	31	54	32.5	776	6	US-10-449-902-5863	Sequence 5863, Ap
	32	54	32.5	1171	8	US-11-266-748A-31634	Sequence 31634, A
	33	54	32.5	1626	9	US-11-218-305-8107	Sequence 8107, Ap
	34	54	32.5	2058	6	US-10-449-902-9041	Sequence 9041, Ap
	35	54	32.5	2123	6	US-10-449-902-21630	Sequence 21630, A
	36	54	32.5	2430	8	US-11-216-545-4043	Sequence 4043, Ap
	37	54	32.5	3000	8	US-11-266-748A-56071	Sequence 56071, A
c	38	54	32.5	88029	8	US-11-270-796-20	Sequence 20, Appl
c	39	54	32.5	164429	8	US-11-266-748A-22662	Sequence 22662, A
	40	53.5	32.2	1517	6	US-10-953-349-16479	Sequence 16479, A
	41	53.5	32.2	1517	8	US-11-216-545-3973	Sequence 3973, Ap

SCORE Search Results Details for Application 10617561 and Search Result us-10-617-561-4.p2n.rst.

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This page gives you Search Results detail for the Application 10617561 and Search Result us-10-617-561-4.p2n.rst.

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:35:25 ; Search time 3516.55 Seconds
(without alignments)
787.138 Million cell updates/sec

Title: US-10-617-561-4
Perfect score: 166
Sequence: 1 FALALKALKKALKKKLKKALKKALQHSYGLRPG 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102055_128/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561@CGN_1_1_17145@runat_11082006_102055_128 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*

2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_hlc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	68	41.0	491	12	CE110244	CE110244 tigr-gss-
	2	67	40.4	812	5	CJ433190	CJ433190 CJ433190
c	3	66.5	40.1	533	12	CE820965	CE820965 tigr-gss-
	4	65.5	39.5	227	1	AV379208	AV379208 AV379208
c	5	65	39.2	488	11	AQ540646	AQ540646 RPCI-11-3
c	6	64	38.6	392	1	AV438464	AV438464 AV438464
	7	64	38.6	411	12	CC153518	CC153518 CSU-K34.1
	8	64	38.6	636	2	BG543264	BG543264 E0758 Chi
c	9	63.5	38.3	526	7	BF511936	BF511936 UI-H-BI4-
c	10	63.5	38.3	734	4	CB243067	CB243067 UI-CF-FN0
	11	63.5	38.3	809	4	BX104967	BX104967 BX104967
	12	63.5	38.3	1776	6	BC067290	BC067290 Homo sapi
	13	63	38.0	153	14	AY399439	AY399439 Pan trogl
	14	63	38.0	291	14	AY399438	AY399438 Homo sapi
	15	63	38.0	291	14	AY399440	AY399440 Mus muscu
	16	63	38.0	306	7	BE411580	BE411580 ISC007.B0
	17	63	38.0	316	1	AJ399430	AJ399430 AJ399430
c	18	63	38.0	395	7	BF511931	BF511931 UI-H-BI4-
	19	63	38.0	402	5	CJ201010	CJ201010 CJ201010
	20	63	38.0	403	5	CJ202177	CJ202177 CJ202177
c	21	63	38.0	421	1	AA043996	AA043996 zk58h08.s
	22	63	38.0	428	12	CG607997	CG607997 OST287671
c	23	63	38.0	440	1	AI014477	AI014477 os34e10.s
	24	63	38.0	483	6	AK139480	AK139480 Mus muscu
	25	63	38.0	494	5	CJ059442	CJ059442 CJ059442
	26	63	38.0	556	9	CX763652	CX763652 AGENCOURT
c	27	63	38.0	611	9	DN051020	DN051020 JGI_CABA6
	28	63	38.0	612	9	DN051021	DN051021 JGI_CABA6
c	29	63	38.0	664	1	AJ737143	AJ737143 AJ737143
	30	63	38.0	734	1	AJ737137	AJ737137 AJ737137
c	31	63	38.0	787	14	CT194654	CT194654 Sus scrof
	32	63	38.0	832	14	CNS03CW8	AL238337 Tetraodon
	33	63	38.0	870	13	DU383234	DU383234 109831307
c	34	63	38.0	942	10	DW019805	DW019805 PMAD-aac0
	35	62.5	37.7	843	7	BF026595	BF026595 601672736
	36	62.5	37.7	877	8	CO463711	CO463711 MZCCL1503
	37	62	37.3	517	3	BP072343	BP072343 BP072343
	38	62	37.3	631	8	CO873883	CO873883 BovGen_02